Amendments to the Claims

Please cancel Claims 22-41 and 43-53. Please amend Claim 42. Please add new Claims 54-65. The Claim Listing below will replace all prior versions of the claims in the application:

Claim Listing

1-41. (Canceled)

42. (Currently amended) A method for determining nucleotide identity of at least one nucleotide position of a polynucleotide of interest, comprising the steps of;

a) contacting said polynucleotide of interest with a population of single-stranded primers, wherein said single-stranded primers comprise an array of one or more sets of one or more oligonucleotides, wherein at least one set comprises at least two oligonucleotides that are substantially homologous but differ from each other by one base at their 3′ termini, wherein the oligonucleotides of the array have known sequence and wherein each oligonucleotide is attached to a solid support at a known location, to form the array, wherein at least one oligonucleotide of the array hybridizes to said polynucleotide of interest immediately adjacent to each nucleotide position to be identified, generating template-single-stranded primer complexes;

b) subjecting said complexes to a single base extension reaction to extend each annealed primer by a terminating nucleotide, generating extended primers; [and]

c) identifying each terminating nucleotide that has been added to each primer; thereby determining the identity of at least one nucleotide position of a polynucleotide of interest; and

d) removing the terminating nucleotides from the annealed primers after completed analysis to prepare the solid support for reuse .

43-53. (Canceled)

54. (New) A method of analyzing a polynucleotide of interest for the presence or absence of an altered region, comprising the steps of:

a) annealing a single sample of the polynucleotide of interest to a plurality of primers, wherein the primers comprise an array of consecutive, single-stranded oligonucleotides having known sequences, wherein each primer differs from the previous primer in the array by one base at the 3' end, and wherein the primers are capable of hybridizing successively along the polynucleotide of interest, generating a plurality of annealed primers;

b) subjecting the plurality of annealed primers to a single base extension reaction to extend each annealed primer by addition of a terminating nucleotide to form a plurality of extended primers; and

c) observing the identity of each terminating nucleotide that has been added to each extended primer,

thereby analyzing the polynucleotide of interest for the presence or absence of an altered region.

55. (New) The method of Claim 54, wherein the single base extension reaction comprises subjecting the plurality of annealed primers to a reaction mixture comprising a polymerase and nucleotides corresponding to each of the four bases.

56. (New) The method of Claim 55, wherein the nucleotides corresponding to each of the four bases are mutually distinguishable.

57. (New) The method of Claims 55, wherein three of the four nucleotides are differently labeled.

58. (New) The method of Claim 57, wherein the three differently labeled nucleotides are fluorescently labeled.

59. (New) The method of Claim 54, further comprising analyzing a polynucleotide that is complementary to the polynucleotide of interest.

60. (New) The method of Claim 54, wherein the terminating nucleotides are dideoxynucleotides.

61. (New) The method of Claim 54, wherein the length N of the plurality of primers is between 7 and 30 inclusive.

62. (New) The method of Claim 54, wherein the length N of the plurality of primers is between 20 and 24 inclusive.

63. (New) The method of Claim 54, wherein the plurality of primers comprises single-stranded oligonucleotides of different lengths.

64. (New) The method of Claim 54, wherein observing the identity and location of the terminating nucleotides comprises use of a charge coupled device or a photomultiplier tube.

65. (New) The method of Claim 54, wherein the terminating nucleotides are dinucleotides.